SEQUENCE LISTING

<110> Young, Karen K. Y.
Roche Molecular Systems, Inc.

<120> Compositions and Methods for Detecting Certain Flaviviruses, Including Members of the Japanese Encephalitis Virus Serogroup

<130> 022101-000230US

<140> US 10/815,480
<141> 2004-03-31

<150> US 60/459,491
<151> 2003-03-31

<150> US 60/552,454
<151> 2004-03-12

<150> US 60/555,530
<151> 2004-03-22

<160> 74

<170> PatentIn Ver. 2.1

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<400> 2
ttccgagacg gttctgaggg cttac 25

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<220>
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<220>
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<222> (8)
<223> n = t or absent

<400> 3
gwaasccnsy crramcysyy tcggrw 26

<210> 4
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<220>
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<220>
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<222> (8)
<223> n = t or absent

<400> 4
gtaagccncy cagaaccgyy tcggaa 26

<210> 5
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<212> DNA
<213> Artificial Sequence

<220>
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<221> modified_base
<222> (8)
<223> n = absent

<400> 5
gaaasccnct crraacygty tcggaa 26

<210> 6
<211> 26
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:Murray Valley encephalitis virus Primer 1

<400> 6
gaaagcctcc cagamccgty tcggaa 26

<210> 7
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
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<400> 7
gtaagccctc agaaccgtct cggaa 25

<210> 8
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:Example Primer 1

<400> 8
gtaagccctc agaaccgtct cggaa 25

<210> 9
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<220>
<223> Description of Artificial Sequence:region of conserved sequence in 3' untranslated region of the genomes of flaviviruses

<400> 9
tctcctagtc tatcccaggt gtcaa 25

<210> 10
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<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:complement to SEQ ID NO:9

<400> 10
agaggatcag atagggtcca cagtt 25

<210> 11
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:Japanese encephalitis virus serogroup Primer 2

<220>
<221> modified_base
<222> (11)
<223> n = t or absent

<400> 11
yccyastmtw nyyccaggtr tcaa 24

<210> 12
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:West Nile virus Primer 2

<400> 12
ycctagtcta tcccaggtrt caa 23

<210> 13
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:Japanese encephalitis virus Primer 2

<400> 13
cccyastmta tyyccaggtg tcaa 24

<210> 14
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:Murray Valley encephalitis virus Primer 2

<400> 14
tcctagtctt ttcccaggtg tcaa 24

<210> 15
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
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<400> 15
tcctagtcta tcccaggtgt caa 23

<210> 16
<211> 28
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:region of conserved sequence in 3' untranslated region of the genomes of flaviviruses

<400> 16
ggactagagg ttagaggaga ccccgcgg 28

<210> 17
<211> 28
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:complement of SEQ ID NO:16

<400> 17
ccgcggggtc tcctctaacc tctagtcc 28

<210> 18
<211> 28
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:probe for detecting flaviviruses

<220>
<221> modified_base
<222> (25)
<223> n = g, c, t, a or absent

<220>
<221> modified_base
<222> (26)
<223> n = c, t, g or absent

<220>
<221> modified_base
<222> (27)
<223> n = g, c, a, t or absent

<220>
<221> modified_base
<222> (28)
<223> n = g, c, a, t or absent

<400> 18
ggwctagwgg ttagaggaga cccynnnn 28

<210> 19
<211> 28
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:probe for detecting Japanese encephalitis virus serogroup members

<400> 19
ggactagwgg ttagaggaga ccccrykk 28

<210> 20
<211> 28
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:probe for detecting West Nile virus

<400> 20
ggactagwgg ttagaggaga ccccrcgk 28

<210> 21
<211> 28
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:probe for detecting Japanese encephalitis virus

<400> 21
ggactagagg ttagaggaga ccccgygg 28

<210> 22
<211> 28
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:probe for detecting Murray Valley encephalitis virus

<400> 22
ggactagagg ttagaggaga ccccactc 28

<210> 23
<211> 29
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:probe for detecting Kunjin virus

<400> 23
aataygtgga ttacatgast tcaytgaag 29

<210> 24
<211> 28
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:probe for
detecting Dengue virus

<400> 24
ggactagagg ttagaggaga ccccyssv 28

<210> 25
<211> 28
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:probe for
detecting yellow fever virus

<400> 25
ggtctagagg ttagaggaga ccctccag 28

<210> 26
<211> 28
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:probe for
detecting Montana myotis leukencephalitis virus

<400> 26
ggactagagg ttagaggaga ccccttcc 28

<210> 27
<211> 28
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:probe for
detecting Modoc virus

<400> 27
ggactagagg ttgagggaga cccccggc 28

<210> 28
<211> 28
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:Example Probe 1

<400> 28
ggactagagg ttagaggaga ccccgcgg 28

<210> 29
<211> 418
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:3' untranlated
region of the genome of St. Louis encephalitis
virus (SLEV) isolate BFS1750

<400> 29
ttgccaccgg atgtcaggta aacggtgctg tctgtaacct ggccccaggt gactgggtta 60
tcaaagccaa tctggccgag tgcaaagccc ctcattccga ctcgggaggg tccctagcac 120
gtaggctgga gaggacgcaa aagtcagacc agaaatgcca cctgaaagca tgctaaaggt 180
gctgtctgta catgccccag gaggactggg ttaacaaagc ttaacagccc cagcggccca 240
aaccatggag tgcgtgacca tggcgtaagg actagaggtt agaggagacc ccgctgcaac 300
ttggcaaggc ccaaacccgc tcgaagctgt agagacgggg gaaggactag aggttagagg 360
agacccttg ccgttaacgc aaacaacagc atattgacac ctggaaagac aggagatc 418

<210> 30
<211> 342
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:3' untranlated
region of the genome of St. Louis encephalitis
virus (SLEV) isolate 1750-Std

<400> 30
ttgccaccgg atgtcaggta aacggtgctg tctgtaacct ggccccaggt gactgggtta 60
tcaaagccaa tctggccgag tgcaaagccc ctcattccga ctcgggaggg tccctagcac 120
gtaggctgga gaggacgcaa aagtcagacc agaaatgcca cctgaaagca tgctaaaggt 180
gctgtctgta catgccccag gaggactggg ttaacaaagc ttaacagccc cagcggccca 240
aaccatggag tgcgtgacca tggcgtaagg actagaggtt agaggagacc ccgcgcaact 300
tggcaaggcc caaacccgct cgaagctgta gagacggggg aa 342

<210> 31
<211> 418
<212> DNA
<213> Artificial Sequence

<220>
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region of the genome of St. Louis encephalitis
virus (SLEV) isolate TD6-4G

<400> 31
ttgccaccgg atgtcaggta aacggtgctg cctgtaacct ggccccaggt gactgggtta 60
tcaaagccaa tctggccgag tgcaaagccc ctcattccga ctcgggaggg tccctggcac 120
gtaggctgga gaggacgcaa aagtcagacc agaaatgcca cctgaaagca tgctaaaggt 180
gctgtctgta catgccccag gaggactggg ttaacaaagc ttaacagccc cagcggccca 240

aaccatggag tgcgtgacca tggcgtaagg actagaggtt agaggagacc ccgctgcaac 300
tcggcaaggc ccaaacccgc tcgaagctgt agagatgggg gaaggactag aggttagagg 360
agacccctttg ccgttaacgc aaacaacagc atattgacac ctggaaagac aggagatc 418

<210> 32
<211> 342
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:3' untranlated
region of the genome of St. Louis encephalitis
virus (SLEV) isolate CoaV750

<400> 32
ttgccaccgg atgtcaggta aacggtgctg cctgtaacct ggccccaggt gactgggtta 60
ccaaagccaa tctggctgag tgcaaagccc ctcgttccga ttcgggaggg tccctggcac 120
gtaggctgga gaggacgcaa aagtcagacc agaaatgcca cctgaaagca tgctaaaggt 180
gctgtctgta catgccccag gaggactggg ttaacaaagc ttaacagccc cagcggccca 240
aaccatggag tgcgtgacca tggcgtaagg actagaggtt agaggagacc ccgcgcaact 300
tggcaaggcc aaaacccgct cgaagctgta gagatggggg aa 342

<210> 33
<211> 418
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:3' untranlated
region of the genome of St. Louis encephalitis
virus (SLEV) isolate L695121.05

<400> 33
ttgccaccgg atgtcaggta aacggtgctg tctgtaacct ggccccaggt gactgggtta 60
tcaaagccaa tccggctggg tgcaaagccc ctcattccga ctcgggaggg tccctggcat 120
gtaggctgga gaggacgcac aagtcagacc agaaatgcca cctgaaagca tgctaaaggt 180
gctgtctgta catgccccag gaggactggg ttaacaaagc ttaacagccc cagcggccca 240
aaccatggag tgcgtgacca tggcgtaagg actagaggtt agaggagacc ccgctgtaac 300
ttggcaaggc ccaaacccgc tcgaagctgt agagacgggg gaaggactag aggttagagg 360
agacccctttg ccgttaacgc aaacaacagc atattgacac ctggaaagac aggagatc 418

<210> 34
<211> 418
<212> DNA
<213> Artificial Sequence

<220>
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region of the genome of St. Louis encephalitis
virus (SLEV) isolate TNM771K

<220>
<221> modified_base
<222> (384)
<223> n = g, a, c or t

<400> 34
ttgccaccgg atgtcaggta aacggtgctg tctgtaacct ggccccaggt gactgggtca 60

tcaaagccaa tctggctggg tgcaaagccc ctcattccga ctcgggaggg tccctggcac 120
gtaggctgga gaggacgcac aagtcagacc agaaatgcca cctgaaagca tgctaaaggt 180
gctgtctgta catgccccag gaggactggg ttaacaaagc ttaacagccc cagcggccca 240
aaccatggag agcgtgacca tggcgtaagg actagaggtt agaggagacc ccgctgtaac 300
ttggcaaggc ccaaacccgc tcgaagctgt agagacgggg gaaggactag aggttagagg 360
agacccctg ccgttaacgc aaanaacagc atattgacac ctggaaagac aggagatc 418

<210> 35
<211> 418
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:3' untranlated
region of the genome of St. Louis encephalitis
virus (SLEV) isolate MSI-7

<400> 35
ttgccaccgg atgtcaggta aacggtgctg tctgtaacct ggccccaggc gactgggtta 60
tcaaagccaa tccggctggg tgcaaagccc ctcattccga ctcgggaggg tccctggcac 120
gtaggctgga gaggacgcac aagtcagacc agaaatgcca cctgaaagca tgctaaaggt 180
gctgtctgta catgccccag gaggactggg ttaacaaagc ttaacagccc cagcggccca 240
aaccatggag tgcgtgacca tggcgtaagg actagaggtt agaggagacc ccgctgtaac 300
ttggcaaggc ccaaacccgc tcaaagctgt agagacgggg gaaggactag aggttagagg 360
agacccctg ccgttaacgc aaacaacagc atattgacac ctggaaagac aggagatc 418

<210> 36
<211> 405
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:3' untranlated
region of the genome of St. Louis encephalitis
virus (SLEV) isolate Kern217

<400> 36
ccggatgtca ggtaaacggt gctgtctgta acctggcccc aggtcactgg gttatcaaag 60
ccaacccggc tgggtgcaaa gcccctcatt ccgactcggg agggtccctg gcacgtaggc 120
tggagaggac gcacaagtca gaccagaaat gccacctgaa agcatgctaa aggtgctgtc 180
tgtacatgcc ccaggaggac tgggttaaca aagcttaaca gccccagcgg cccaaaccat 240
ggagtgcgtg accatggcgt aaggactaga ggttagagga gaccccgctg taacttggca 300
aggcccaaac ccgctcaaag ctgtagagac gggggaagga ctagaggtta gaggagaccc 360
cttgccgtta acgcaaacaa cagcatattg acacctggaa agaca 405

<210> 37
<211> 375
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:3' untranlated
region of the genome of St. Louis encephalitis
virus (SLEV) isolate CoaV608

<400> 37
cccaggcgac tgggttatca aagccaatcc ggctgggtgc aaagcccctc attccgactc 60
gggagggtcc ctggcacgta ggctggagag gacgcacaag tcagaccaga aatgccacct 120

gaaagcatgc taaaggtgct gtctgtacat gccccaggag gactgggtta acaaagctta 180
acagccccag cggcccaaac catggagtgc gtgaccatgg cgtaaggact agaggttaga 240
ggagaccccg ctgtaacttg gcaaggccca aacccgctca aagctgtaga gacgggggaa 300
ggactagagg ttagaggaga ccccttgccg ttaacgcaaa caacagcata ttgacacctg 360
gaaagacagg agatc 375

<210> 38
<211> 411
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:3' untranlated
region of the genome of St. Louis encephalitis
virus (SLEV) isolate TBH-28

<400> 38
ttgccaccgg atgtcaggta aacggtgctg tctgtaacct ggccccaggt gactgggtta 60
tcaaagccaa cccggctggg tgcaaagccc ctcattccga ctcgggaggg tccctggcac 120
gtaggccgga gaggacgcac aagtcagacc agaaatgcca cctgaaagca tgctaaaggt 180
gctgtctgta catgccccag gaggactggg ttaacaaagc ttaacagccc cagcggccca 240
aaccatggag tgcgtgacca tggcgtaagg actagaggtt agaggagacc ccgctgtaat 300
ttggcaaggc ccaaacccgc tcgaagctgt agagacgggg gaaggactag aggttagagg 360
agacccctg ccgttaacgc aaacaacagc atattgacac ctggaaagac a 411

<210> 39
<211> 402
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:3' untranlated
region of the genome of St. Louis encephalitis
virus (SLEV) isolate VR1265

<400> 39
ccggaagtca ggtaaacggt gctgtctgta acctggcccc aggtgactgg gttatcaaag 60
ccaatctggc tgggtgcaaa gcccctcatt ccgactcggg agggtccctg gcacgtaggc 120
tggagcggac gcacaagtca gaccagaaat gccacctgaa agcatgctaa aggtgctgtc 180
tgtacatgcc ccaggaggac tgggttaaca aagcttaaca gccccagcgg cccaaaccat 240
ggagtgcgtg accatggcgt aaggactaga ggttagagga gaccccgctg taacttggca 300
aggcccaaac ccgctcgaag ctgtagagac gggggaagga ctagaggtta gaggagaccc 360
cttgccgtca acgcaaacaa cagcatattg acacctggaa ag 402

<210> 40
<211> 374
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:3' untranlated
region of the genome of St. Louis encephalitis
virus (SLEV) isolate CoaV353

<400> 40
cccaggtgac tgggttatca aagccaatct agctgagtgc aaagcccctc attccgactc 60
gggagggtcc ctggcacgta ggctggagag gacgcaaaag tcagaccaga aatgccacct 120
gaaagcatgc taaaggtgct gtctgtacat gccccaggag gactgggtta acaaagctta 180

acagccccag cggcccaaac catggagtgc gtgaccatgg cgtaaggact agaggttaga 240
ggagaccccg ctgcaacttg gcaaggccca aacccgctcg aagctgtaga gacgggggaa 300
ggactagagg ttagaggaga ccccttgccg ttaacgcaaa caacagcata ttgacacctg 360
gaaagacagg agat 374

<210> 41
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:Dengue virus
consensus upstream primer

<400> 41
gagccccgtc caaggacgta aaaagaa 27

<210> 42
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:Dengue virus
consensus upstream primer

<220>
<221> modified_base
<222> (27)
<223> n = t-butyl-benzyl-dA

<400> 42
gagccccgtc caaggacgta aaaagan 27

<210> 43
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:Dengue virus
consensus upstream primer

<220>
<221> modified_base
<222> (26)
<223> n = methyl-dA

<220>
<221> modified_base
<222> (27)
<223> n = t-butyl-benzyl-dA

<400> 43
gagccccgtc caaggacgta aaaagnn 27

<210> 44
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:Dengue virus
type I upstream primer

<400> 44
gagccccgtc caaggacgta aaatgaa 27

<210> 45
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:Dengue virus
type I upstream primer

<220>
<221> modified_base
<222> (27)
<223> n = t-butyl-benzyl-dA

<400> 45
gagccccgtc caaggacgta aaatgan 27

<210> 46
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:Dengue virus
type I upstream primer

<220>
<221> modified_base
<222> (26)
<223> n = methyl-dA

<220>
<221> modified_base
<222> (27)
<223> n = t-butyl-benzyl-dA

<400> 46
gagccccgtc caaggacgta aaatgnn 27

<210> 47
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:Dengue virus
types II and III upstream primer

<400> 47
gagccccgtc caaggacgtt aaaagaa 27

<210> 48
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:Dengue virus
types II and III upstream primer

<220>
<221> modified_base
<222> (27)
<223> n = t-butyl-benzyl-dA

<400> 48
gagccccgtc caaggacgtt aaaagan 27

<210> 49
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:Dengue virus
types II and III upstream primer

<220>
<221> modified_base
<222> (26)
<223> n = methyl-dA

<220>
<221> modified_base
<222> (27)
<223> n = t-butyl-benzyl-dA

<400> 49
gagccccgtc caaggacgtt aaaagnn 27

<210> 50
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:Dengue virus
type IV upstream primer

<400> 50
attgaagtca ggccacttgt gcca 24

<210> 51
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:Dengue virus
type IV upstream primer

<220>
<221> modified_base
<222> (24)
<223> n = t-butyl-benzyl-dA

<400> 51
attgaagtca ggccacttgt gccn 24

<210> 52
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:Dengue virus
type IV upstream primer

<220>
<221> modified_base
<222> (23)
<223> n = ethyl-dC

<220>
<221> modified_base
<222> (24)
<223> n = t-butyl-benzyl-dA

<400> 52
attgaagtca ggccacttgt gcnn 24

<210> 53
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:Dengue virus
downstream primer

<400> 53
gatctctggt ctttcccagc gtcaa 25

<210> 54
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:Dengue virus
downstream primer

<220>
<221> modified_base
<222> (25)
<223> n = t-butyl-benzyl-dA

<400> 54
gatctctggt ctttcccagc gtcan 25

<210> 55
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:Dengue virus
downstream primer

<220>
<221> modified_base
<222> (24)
<223> n = methyl-dA

<220>
<221> modified_base
<222> (25)
<223> n = t-butyl-benzyl-dA

<400> 55
gatctctggt ctttcccagc gtcnn 25

<210> 56
<211> 28
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:yellow fever
virus upstream primer

<400> 56
aaccgggata aaaactacgg gtggagaa 28

<210> 57
<211> 28
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:yellow fever
virus upstream primer

<220>
<221> modified_base
<222> (28)
<223> n = t-butyl-benzyl-dA

<400> 57
aaccgggata aaaactacgg gtggagan 28

<210> 58
<211> 28
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:yellow fever virus upstream primer

<220>
<221> modified_base
<222> (27)
<223> n = methyl-dA

<220>
<221> modified_base
<222> (28)
<223> n = t-butyl-benzyl-dA

<400> 58
aaccgggata aaaactacgg gtggagnn 28

<210> 59
<211> 26
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:yellow fever virus upstream primer

<400> 59
ataaaaacta cgggtggaga accgga 26

<210> 60
<211> 26
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:yellow fever virus upstream primer

<220>
<221> modified_base
<222> (26)
<223> n = t-butyl-benzyl-dA

<400> 60
ataaaaacta cgggtggaga accggn 26

<210> 61
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:yellow fever
virus downstream primer

<400> 61
actccggtct ttccctggcg tcaa 24

<210> 62
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:yellow fever
virus downstream primer

<220>
<221> modified_base
<222> (24)
<223> n = t-butyl-benzyl-dA

<400> 62
actccggtct ttccctggcg tcan 24

<210> 63
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:yellow fever
virus downstream primer

<220>
<221> modified_base
<222> (23)
<223> n = methyl-dA

<220>
<221> modified_base
<222> (24)
<223> n = t-butyl-benzyl-dA

<400> 63
actccggtct ttccctggcg tcnn 24

<210> 64
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:St Louis
encephalitis virus upstream primer

<400> 64
caaagcccct cattccgact cggga 25

<210> 65
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:St Louis
encephalitis virus upstream primer

<220>
<221> modified_base
<222> (25)
<223> n = t-butyl-benzyl-dA

<400> 65
caaagcccct cattccgact cgggn 25

<210> 66
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:St Louis
encephalitis virus upstream primer

<400> 66
tctcctgtct ttccaggtgt caa 23

<210> 67
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:St Louis
encephalitis virus upstream primer

<220>
<221> modified_base
<222> (23)
<223> n = t-butyl-benzyl-dA

<400> 67
tctcctgtct ttccaggtgt can 23

<210> 68
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:St.Louis
encephalitis virus (SLEV) first primer complement

<400> 68
ttgacacctg gaaagacagg aga 23

<210> 69
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:St.Louis
encephalitis virus (SLEV) second primer

<400> 69
caaagcccct cattccgact cggg 24

<210> 70
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:flavivirus
anti-sense probe

<400> 70
gggtctcctc taacctctag tccttccccc 30

<210> 71
<211> 98
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:region of
conserved sequence in 3' untranslated region of
the genome of flavivirus AF196835

<400> 71
caaccccagg aggactgggt gaacaaagcc gcgaagtgat ccatgtaagc cctcagaacc 60
gtctcggaag gaggacccca catgttgtaa cttcaaag 98

<210> 72
<211> 105
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:region of
conserved sequence in 3' untranslated region of
the genome of flavivirus AF196835

<400> 72
tgactgaagc tgtaggtcag gggaaggact agaggttagt ggagaccccg tgccacaaaa 60
caccacaaca aaacagcata ttgacacctg ggatagacta ggaga 105

<210> 73
<211> 121
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:region of
conserved sequence in 3' untranslated region of
the genome of flavivirus AF196835

<400> 73
cagggcgaaa ggactagagg ttagaggaga ccccgcggtt taaagtgcac ggcccagcct 60
gactgaagct gtaggtcagg ggaaggacta gaggttagtg gagaccccgt gccacaaaac 120
a 121

<210> 74
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:Example Primer 2

<400> 74
tctcctagtc tatcccaggt gtcaa 25